



REPLACEMENT SHEETS (FIGS. 1-5)

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Figure 1

2588 GA TCAATCGCAT TCATTTTAAG AAATTATACC TTTTGTAGTAC TTGCTGAAGA
2641 ATGATTCAGG GTAAATCACA TACTTTGTTT AGAGAGGCGA GGGGTTTAAC CCGAGTCACC
2701 CAGCTGGTCT CATA CATAGA CAGCACTTGT GAAGGATTGA ATGCAGGTTT CAGGTGGAGG
2761 GAAGACGTGG ACACCATCTC CACTGAGCCA TGCAGACATT TTTAAAAGCT ATACACAAAA
2821 TTGTGAGAAG ACATTGGCCA ACTCTTTCAA AGTCTTTCTT TTTCCACGTG CTTCTTATTT
2881 TAAGCGAAAT ATATTGTTTG TTTCTTCTA AAAAAAAAAA 2890

Figure 2a

1 CAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCTCTGATCCTGATC 60
61 TCTGTTCCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC 120
121 ATGCCCTCTGCAGGAACACTTCTTGGGTTTCAGGGGATTATCTGTAATGCCAACAAACCCC 180
1 M P S A G T L P W V Q G I I C N A N N P 20
181 TGTTTCCGTTACCCGACTCCTGGGGAGGCTCCCGAGTTGTTGGAAACTTTAACAAATCC 240
21 C F R Y P T P G E A P G V V G N F N K S 40
241 ATTGTGGCTCGCCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAAAGACACC 300
41 I V A R L F S D A R R L L L Y S Q K D T 60
301 AGCATGAAGGACATGCGCAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA 360
61 S M K D M R K V L R T L Q Q I K K S S S 80
361 AACTTGAAGCTTCAAGATTTCTGTTGGTGGACAATGAAACCTTCTCTGGGTTCTGTATCAC 420
81 N L K L Q D F L V D N E T F S G F L Y H 100
421 AACCTCTCTCTCCCAAAGTCTACTGTGGACAAGATGCTGAGGGCTGATGTCATTCTCCAC 480
101 N L S L P K S T V D K M L R A D V I L H 120
481 AAGGTATTTTGTCAAGGCTACCAAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 540
121 K V F L Q G Y Q L H L T S L C N G S K S 140
541 GAAGAGATGATTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCCTACCAAGGGAG 600
141 E E M I Q L G D Q E V S E L C G L P R E 160
601 AAAGTGGCTGCAGCAGAGCGAGTACTTCGTTCCAACATGGACATCCTGAAGCCAATCCTG 660
161 K L A A A E R V L R S N M D I L K P I L 180
661 AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCCGAAGCCACAAAAACA 720
181 R T L N S T S P F P S K E L A E A T K T 200
721 TTGCTGCATAGTCTTGGGACTCTGGCCCAGGAGCTGTTTCTGAGCATGAGAAGCTGGAGTGAC 780
201 L L H S L G T L A Q E L F S M R S W S D 220
781 ATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC 840
221 M R Q E V M F L T N V N S S S S S T Q I 240
841 TACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGGGGCTGAAGATCAAG 900
241 Y Q A V S R I V C G H P E G G G L K I K 260
901 TCTCTCAACTGGTATGAGGACAACAACACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 960
261 S L N W Y E D N N Y K A L F G G N G T E 280

Figure 2b

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961 GAAGATGCTGAAACCTTCTATGACAACTCTACAACCTCCTTACTGCAATGATTTGATGAAG 1020
281 E D A E T F Y D N S T T P Y C N D L M K 300
1021 AATTTGGAGTCTAGTCCTCTTTCCCGCATTATCTGGAAAGCTCTGAAGCCGCTGCTCGTT 1080
301 N L E S S P L S R I I W K A L K P L L V 320
1081 GGGAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCATGGCTGAGGTGAAC 1140
321 G K I L Y T P D T P A T R Q V M A E V N 340
1141 AAGACCTTCCAGGAAGTGGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAAGTCAAGC 1200
341 K T F Q E L A V F H D L E G M W E E L S 360
1201 CCCAAGATCTGGACCTTCATGGAGAAGAGCCAAAGAAATGGACCTTGTCCGGATGCTGTTG 1260
361 P K I W T F M E N S Q E M D L V R M L L 380
1261 GACAGCAGGGACAATGACCACTTTTGGGAACAGCAAGTGGATGGCTTAGATTGGACAGCC 1320
381 D S R D N D H F W E Q Q L D G L D W T A 400
1321 CAAGACATCGTGGCGTTTTTGGCCAAGCAGCCAGAGGATGTCCAGTCCAGTAATGGTTCT 1380
401 Q D I V A F L A K H P E D V Q S S N G S 420
1381 GTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCAGGCAATCCGGACCATATCTCGC 1440
421 V Y T W R E A F N E T N Q A I R T I S R 440
1441 TTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCCATAGCAACAGAAGTCTGGCTCATC 1500
441 F M E C V N L N K L E P I A T E V W L I 460
1501 AACAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTGTTCACTGGA 1560
461 N K S M E L L D E R K F W A G I V F T G 480
1561 ATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGATCCGAATGGACATT 1620
481 I T P G S I E L P H H V K Y K I R M D I 500
1621 GACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACCCTGGTCCTCGAGCT 1680
501 D N V E R T N K I K D G Y W D P G P R A 520
1681 GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG 1740
521 D P F E D M R Y V W G G F A Y L Q D V V 540
1741 GAGCAGGCAATCATCAGGGTGCTGACGGGCACCGAGAAGAAAAGTGGTGTCTATATGCAA 1800
541 E Q A I I R V L T G T E K K T G V Y M Q 560
1801 CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGAGCCGGTCAATG 1860
561 Q M P Y P C Y V D D I F L R V M S R S M 580
1861 CCCCTCTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG 1920
581 P L F M T L A W I Y S V A V I I K G I V 600
1921 TATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGCATC 1980
601 Y E K E A R L K E T M R I M G L D N S I 620
1981 CTCTGGTTTAGCTGGTTTATTAGTAGCCTCATTCTCTTCTTGTGAGCGCTGGCCTGCTA 2040
621 L W F S W F I S S L I P L L V S A G L L 640
2041 GTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTGTC 2100
641 V V I L K L G N L L P Y S D P S V V F V 660
2101 TTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTC 2160

Figure 2c

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661 F L S V F A V V T I L Q C F L I S T L F 680
2161 TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC 2220
681 S R A N L A A A C G G I I Y F T L Y L P 700
2221 TACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC 2280
701 Y V L C V A W Q D Y V G F T L K I F A S 720
2281 CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGAGCAG 2340
721 L L S P V A F G F G C E Y F A L F E E Q 740
2341 GGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCTGTGGAGGAAGATGGCTTCAAT 2400
741 G I G V Q W D N L F E S P V E E D G F N 760
2401 CTCACCACTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG 2460
761 L T T S V S M M L F D T F L Y G V M T W 780
2461 TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATTCCCAGGCCCTGGTATTTTCTTGC 2520
781 Y I E A V F P G Q Y G I P R P W Y F P C 800
2521 ACCAAGTCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACCCTGGTTCCAACCAG 2580
801 T K S Y W F G E E S D E K S H P G S N Q 820
2581 AAGAGAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC 2640
821 K R I S E I C M E E E P T H L K L G V S 840
2641 ATTCAGAACCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCTGTTCGATGGCCTGGCA 2700
841 I Q N L V K V Y R D G M K V A V D G L A 860
2701 CTGAATTTTATGAGGGCCAGATCACCTCCTTCCTGGGCCACAATGGAGCGGGGAAGACG 2760
861 L N F Y E G Q I T S F L G H N G A G K T 880
2761 ACCACCATGTCAATCCTGACCGGGTGTTCCTTCCTGGGCCACCTCGGGCACCGCCTACATCTG 2820
881 T T M S I L T G L F P P T S G T A Y I L 900
2821 GGAAAAGACATTGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCCAG 2880
901 G K D I R S E M S T I R Q N L G V C P Q 920
2881 CATAACGTGCTGTTTGACATGCTGACTGTGGAAGAACACATCTGGTTCTATGCCCCGCTTG 2940
921 H N V L F D M L T V E E H I W F Y A R L 940
2941 AAAGGGCTCTCTGAGAAGCACGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3000
941 K G L S E K H V K A E M E Q M A L D V G 960
3001 TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCAGGTGGAATGCAGAGAAAAG 3060
961 L P S S K L K S K T S Q L S G G M Q R K 980
3061 CTATCTGTGGCCTTGGCCTTTGTCTGGGGGATCTAAGGTTGTCAATTCTGGATGAACCCACA 3120
981 L S V A L A F V G G S K V V I L D E P T 1000
3121 GCTGGTGTGGACCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA 3180
1001 A G V D P Y S R R G I W E L L L K Y R Q 1020
3181 GGCCGCACCATTTATTCTCTCTACACACCACATGGATGAAGCGGACGTCTCTGGGGGACAGG 3240
1021 G R T I I L S T H H M D E A D V L G D R 1040
3241 ATTGCCATCATCTCCCATGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC 3300
1041 I A I I S H G K L C C V G S S L F L K N 1060
3301 CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT 3360

Figure 2d

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1061 Q L G T G Y Y L T L V K K D V E S S L S 1080
3361 TCCTGCAGAAACAGTAGTAGCACTGTGTACATACCTGAAAAAGGAGGACAGTGTCTCTCAG 3420
1081 S C R N S S S T V S Y L K K E D S V S Q 1100
3421 AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC 3480
1101 S S S D A G L G S D H E S D T L T I D V 1120
3481 TCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCCGGCTGGTGGAAGACATA 3540
1121 S A I S N L I R K H V S E A R L V E D I 1140
3541 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTTGTGGAA 3600
1141 G H E L T Y V L P Y E A A K E G A F V E 1160
3601 CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 3660
1161 L F H E I D D R L S D L G I S S Y G I S 1180
3661 GAGACGACCCTGGAAGAAATATTCTCAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG 3720
1181 E T T L E E I F L K V A E E S G V D A E 1200
3721 ACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCGGGGACAAGCAGAGC 3780
1201 T S D G T L P A R R N R R A F G D K Q S 1220
3781 TGTCTTCGCCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATTCTGACATAGACCCA 3840
1221 C L R P F T E D D A A D P N D S D I D P 1240
3841 GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGTCTACCAGGTGAAA 3900
1241 E S R E T D L L S G M D G K G S Y Q V K 1260
3901 GGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTGCC 3960
1261 G W K L T Q Q Q F V A L L W K R L L I A 1280
3961 AGACGGAGTCGGAAAGGATTTTTTGTCTCAGATTGTCTTGCCAGCTGTGTTTGTCTGCATT 4020
1281 R R S R K G F F A Q I V L P A V F V C I 1300
4021 GCCCTTGTGTTTCAAGCCTGATCGTGCCACCCTTTGGCAAGTACCCCAGCCTGGAACCTCAG 4080
1301 A L V F S L I V P P F G K Y P S L E L Q 1320
4081 CCCTGGATGTACAACGAACAGTACACATTTGTGAGCAATGATGCTCCTGAGGACACGGGA 4140
1321 P W M Y N E Q Y T F V S N D A P E D T G 1340
4141 ACCCTGGAACCTCTTAAACGCCCTCACCAAAGACCCTGGCTTCGGGACCCGCTGTATGGAA 4200
1341 T L E L L N A L T K D P G F G T R C M E 1360
4201 GGAAACCCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCA 4260
1361 G N P I P D T P C Q A G E E E W T T A P 1380
4261 GTTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACTGGACAATGCAGAACCTTCA 4320
1381 V P Q T I M D L F Q N G N W T M Q N P S 1400
4321 CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCAGGG 4380
1401 P A C Q C S S D K I K K M L P V C P P G 1420
4381 GCAGGGGGGCTGCCTCCTCCACAAAGAAAACAAACACTGCAGATATCCTTCAGGACCTG 4440
1421 A G G L P P P Q R K Q N T A D I L Q D L 1440
4441 ACAGGAAGAAACATTTTCGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC 4500
1441 T G R N I S D Y L V K T Y V Q I I A K S 1460
4501 TTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCACT 4560

Figure 2e

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1461 L K N K I W V N E F R Y G G F S L G V S 1480
4561 AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAA 4620
1481 N T Q A L P P S Q E V N D A T K Q M K K 1500
4621 CACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGAAGATTT 4680
1501 H L K L A K D S S A D R F L N S L G R F 1520
4681 ATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCAT 4770
1521 M T G L D T R N N V K V W F N N K G W H 1540
4741 GCAATCAGCTCTTTCTGAATGTCAACAATGCCATTCTCCGGGGCCAACTGCAAAAG 4800
1541 A I S S F L N V I N N A I L R A N L Q K 1560
4801 GGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCTGAATCTCACCAAG 4860
1561 G E N P S H Y G I T A F N H P L N L T K 1580
4861 CAGCAGCTCTCAGAGGTGGCTCCGATGACCACATCAGTGGATGTCCTTGTGTCCATCTGT 4920
1581 Q Q L S E V A P M T T S V D V L V S I C 1600
4921 GTCATCTTTGCAATGTCCTTCGTCCCAGCCAGCTTTGTCTGATTCTGATCCAGGAGCGG 4980
1601 V I F A M S F V P A S F V V F L I Q E R 1620
4981 GTCAGCAAAGCAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTC 5040
1621 V S K A K H L Q F I S G V K P V I Y W L 1640
5041 TCTAATTTTGTCTGGGATATGTGCAATTAGCTTGTCCCTGCCACACTGGTCATTATCATC 5100
1641 S N F V W D M C N Y V V P A T L V I I I 1660
5101 TTCATCTGCTTCCAGCAGAAGTCCTATGTGTCTCCACCAATCTGCCTGTGCTAGCCCTT 5160
1661 F I C F Q Q K S Y V S S T N L P V L A L 1680
5161 CTACTTTTGTCTGTATGGGTGGTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTT 5220
1681 L L L L Y G W S I T P L M Y P A S F V F 1700
5221 AAGATCCCCAGCACAGCCTATGTGGTGCTCACCAGCGTGAACCTCTTCATTGGCATTAAAT 5280
1701 K I P S T A Y V V L T S V N L F I G I N 1720
5281 GGCAGCGTGGCCACCTTTGTGCTGGAGCTGTTACCCGACAATAAGCTGAATAATATCAAT 5340
1721 G S V A T F V L E L F T D N K L N N I N 1740
5341 GATATCCTGAAGTCCGTGTTCTTGATCTTCCACATTTTTGCCTGGGACGAGGGCTCATC 5400
1741 D I L K S V F L I F P H F C L G R G L I 1760
5401 GACATGGTGAAAAACCAGGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTT 5460
1761 D M V K N Q A M A D A L E R F G E N R F 1780
5461 GTGTCACCATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGG 5520
1781 V S P L S W D L V G R N L F A M A V E G 1800
5521 GTGGTGTCTTCTCATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCCAGACCT 5580
1801 V V F F L I T V L I Q Y R F F I R P R P 1820
5581 GTAAATGCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGGCGGGAAAGACAG 5640
1821 V N A K L S P L N D E D E D V R R E R Q 1840
5641 AGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATA 5700
1841 R I L D G G G Q N D I L E I K E L T K I 1860
5701 TATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCATTCTCCTGGTGAG 5760

Figure 2f

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1861 Y R R K R K P A V D R I C V G I P P G E 1880
 5761 TGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAAAATCATCAACTTTCAAGATGTTAACA 5820
 1881 C F G L L G V N G A G K S S T F K M L T 1900
 5821 GGAGATAACCACTGTTACCAGAGGAGATGCTTTCCTTAACAGAAATAGTATCTTATCAAAC 5880
 1901 G D T T T V T R G D A F L N R N S I L S N 1920
 5881 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTG 5940
 1921 I H E V H Q N M G Y C P Q F D A I T E L 1940
 5941 TTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAA 6000
 1941 L T G R E H V E F F A L L R G V P E K E 1960
 6001 GTTGGCAAGGTTGGTGAGTGGGCGATTGCGAAACTGGGCCTCGTGAAGTATGGAGAAAAA 6060
 1961 V G K V G E W A I R K L G L V K Y G E K 1980
 6061 TATGCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6120
 1981 Y A G N Y S G G N K R K L S T A M A L I 2000
 6121 GGCGGGCCTCCTGTGGTGTCTTCTGGATGAACCCACCACAGGCATGGATCCCAAAGCCCCGG 6180
 2001 G G P P V V F L D E P T T G M D P K A R 2020
 6181 CGGTTCTTGTGGAATTGTGCCCTAAGTGTGTCAAGGAGGGGAGATCAGTAGTGCTTACA 6240
 2021 R F L W N C A L S V V K E G R S V V L T 2040
 6241 TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA 6300
 2041 S H S M E E C E A L C T R M A I M V N G 2060
 6301 AGGTTTCAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACA 6360
 2061 R F R C L G S V Q H L K N R F G D G Y T 2080
 6361 ATAGTTGTACGAATAGCAGGGTCCAACCCGGACCTGAAGCCTGTCCAGGATTTCTTTGGA 6420
 2081 I V V R I A G S N P D L K P V Q D F F G 2100
 6421 CTTGCATTTCTCCTGGAAGTGTTCAAAAGAGAAAACACCGGAACATGCTACAATACCAGCTT 6480
 2101 L A F P G S V P K E K H R N M L Q Y Q L 2120
 6481 CCATCTTCATTATCTTCTCTGGCCAGGATATTTCAGCATCCTCTCCCAGAGCAAAAAGCGA 6540
 2121 P S S L S S L A R I F S I L S Q S K K R 2140
 6541 CTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACCTT 6600
 2141 L H I E D Y S V S Q T T L D Q V F V N F 2160
 6601 GCCAAGGACCAAAGTGATGATGACCACTTAAAGACCTCTCATTACACAAAAACCAGACA 6660
 2161 A K D Q S D D D H L K D L S L H K N Q T 2180
 6661 GTAGTGGACGTTGCAGTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAAGAAAGCTAT 6720
 2181 V V D V A V L T S F L Q D E K V K E S Y 2200
 6721 GTATGAAGAATCCTGTTTCATACGGGGTGGCTGAAAGTAAAGAGGGACTAGACTTTCCTTT 6780
 2201 V *
 6781 GCACCATGTGAAGTGTGTGGAGAAAAGAGCCAGAAGTTGATGTGGGAAGAAGTAAACTG 6840
 6841 GATACTGTACTGATACTATTCAATGCAATGCAATTCAATG 6880

Figure 3

5' 1 GTACCCCCCT TGCCTGGTTG ATCCTCAGGG TTCTACTTAG AATGCCTCGA

Figure 3a

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51 AAAGTCTTGG CTGGACACCC ATGCCCAGTC TTTCTGCAGG GTCCCATTGG
101 GGTTAACCTT CTCATTTTCAT CCCATGTGAA CCAGGCCAGG CCCATCAGGG
151 TTTGGCAACC CCCTGATGCA GTGGTTGCTG CCAGGTGACA GGAGCAAGCC
201 TGCAGCTGCT GGGGGGCCAT GCAGAGACAG CCTGCCAGAG GGGAGACCAC
251 CTGGGGAGGC CAGAGCCGTG GAGACAGCAA GAGACCAGGG GCTGAGGACA
301 GAGTAGTACA GGTCTTTGGT CCCAGTAGTC CTGAAACCAC TGCACCTCCGA
351 ACCTTTCTGT ACTTAGCTTA AGCCAGTTGG AGTTTCTGTC CTTTACAACC
401 AAGAGCCTTG ATAGGAATGG GGTCTGTGTC TACGCTACTG TTGGCTTCTT
451 TCCCGATCGG GCGCTGGAGG GGAACACAGC AGTGACTACA GTGGGATGCT
501 TACTCGGTGC TGGGCATGCT AGAAAGTGCT TGCCATGCCT TATTTCCAC
551 GTGGTGGGGA TTTTGACCCC ACCTGTACAG ACAGATAAGT GAGGACCCCTT
601 TTCACCTTAT CCTGCAACAG AAAATCCAGC AGCCAAAGCC AACAAAGGGCC
651 CAGCATAGCA TCTTCCCTCT CTGACTTCAT CCTCACGCTC CACACACCAT
701 CCCCCTGGCC ATTCCCAGCA GCCCAGTAAG CACTGCCTCA CACTTCCAGT
751 TCCGGACCAG CCAGGATGGC CAGGCTGGAT GGGGGCCATC CACCGGCTGA
801 AGCCAATTGC CTATTCTCGA GCTGAAGGTG AATCAATCCC GCATAAATCT
851 TCGGGCAGAG AACTNGGGTG GGGGGTAGAA GAGGGGGAAT GTCTAGAAGG
901 AAATTCTGGG GCACATTCCT GGAAGTGAGG AGGATGGATA TTGGACAGAA
951 ATTATGTCAT TGCAGGCACC CTCACTTGCC CTGGCCACAT GGACAGTTCC
1001 TCCCCGGCTG TGTTCCGNGC CTCCTCTCGT GCTCCAGGGC CTGTCTGTTT
1051 CTGGAGCGAG ATGGGTCCCA GGGCTGGGCA CCAGTCCCCA TCTCCAGCCA
1101 TCAGGCACTT TCCTCTCTGT GTTTTGGCGT AAACACNTCC CTAGGTTTGT
1151 GGATCTGAAT CCTCTTCCCA ACACACTCAA GCTTTGCTGG GCCTCCCTGC
1201 AGTGTATGTT TAAGGCACCA CACAGCCTCC AAGGCCTGGC ACCCGGGCAG
1251 TGGCCACCTG GTAAACACAG CAGTCAGATT TCCTCATTTT AGCCAAGTGT
1301 AAAATCAAGG TAATGGATCT ACNCTTTTTT TTTTNTNTTT TTTCCAGGGG
1351 GNTNNTTTTT TTTTGAGACG GAGTCTCACT CTGTCANCCC CGGTCTGGAG
1401 TGCAGTGGCT CAATCTCGGC TCANCTGGCA AGCTCCGCCT CCCAGGTTCA
1451 TGCCATTCTC CTGCCTCAGC CTACATAGTA GCTGGGACTA CAGGTGCCCCG
1501 CCACCACACC TAGCTAATTT TTTGTATTTT TAGTAGAGAC GGGGTTTCAT
1551 CATGTTAGCC AGGATGGTCT CGATCTCCTG ACCTCCCAA GTGGTGGGAG
1601 TTACAGGTGT GAGCCACTGC GCNCCGGCTG GATGACTCTT GAGACAACAC
1651 CATTGAGACA AAGGCAAGGC CTCCCACTTA AACTCATAAC CGTGTCTCCT
1701 TTCTCTCCTT CGATTTGAGC GGCTGAATTT GGTACAGTC ATCTGACCTG
1751 TGGGTGTGAA NGTCCACCTG CCTGGCATAA AAAGCTGTGC CTCCTTTCTA
1801 GGTGAGGAGA AAGAGAGAGA CCTGGCTCAT CTGAGGTGTG GTTGGGAGGG
1851 GGGACCCAGG TGTGCTGGAA ATGAAAAGAA ATGCATTCTT GTTTTTTCGT
1901 CCCAACATGC AAACAACCTGA ACAAAGCAT TAGGGCCTGA GACTGGGAGT
1951 AAAGAATTCC TTGTCACCAT GGATACCAGG AAATGGCCCC ACTTATATAT
2001 AATAAGGGCT TTAGAGATGC TGGACCATCT GATATTCCAG CCTGGGGCCA
2051 CATGGGAGTG TGCCCTGGTG TTATTCCTTA TACAGTTCCA TGAACATGGC
2101 TCTGGAAACA CCTCTGTCTG CAGAAAATGA GGCTTTTCTT TTTTGTTCG

Figure 3b

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2151 GGGGTGAACA GAGGGCAGAG GCCTGGGCAT CTTCACTCAG CACCCCTTTG
 2201 TAACCCAGCA CTTAGCACCA TGGCTGGCGC ACAGCAATGT CACATGTGTG
 2251 AGTGCACACG ATGCCTCACT GCCAGGGGTC ACCCCACACC GGTGCTGTTG
 2301 GGGGCGTTGG AGTGGTTATC TCTTCTTTAG TCCTCAAGCT CCTACCTGGC
 2351 AGAGAGCTGC CCAACACCGT CGGGGTGGGG TGGGCGGGAA GGGGAAGAAGC
 2401 AGCAGCAAGA AAGAAGCCCC CTGGCCCTCA CTCTCCCTCC CTGGACGCCC
 2451 CCTCTTCGAC CCCATCACAC AGCCGCTTGA GCCTTGGAGN CAGTGGATTT
 2501 CCGAGCCTGG GAACCCCCGG CGTCTGTCCC GGTGTCCCCC GCAGCCTCAC
 2551 CCNCGTGCTG GCCCAGCCCC CGCGAGTTCG GGACCCGGGG TTTCCGGGGT
 2601 GGCAGGGGGT TCCCATGCCG CCTGCGAGGC CTCGGCTCGG GCCGCTCCCC
 2651 GAACCTGCAC TTCAGGGGTC CTGGTCCGCC GCCCCAGCA GGAGCAAAAC
 2701 AAGAGCACGC GCACCTGCCG GCCCGCCCGC CCCCTTGGTG CCGGCCAATC
 2751 GCGCGCTCGG GCGGGGGTCG GCGCGCTGG AACCAGAGCC GGAGCCGGAT
 2801 CCCAGCCGGA GCCCAAGCGC AGCCCGCACC CCGCGCAGCG GCTGAGCCGG
 2851 GAGCCAGCGC AGCCTCGGCC CCGCAGCTCA AGCCTCGTCC CCGCCGCCNG
 2901 CCGCCGCACG CCGCCGCCCG CGCCCCGGG GCATGGCTGT CTGATGGCCG

EXON1/INTRON 1

2951 CTTTCTCGGT CGGCACCGCC ATGGTGAGTG AGCGCATCCT TCGTCCGCCG
 3001 GGAACGGTTT TATTTTCAAG GAGAGCAGGA AACACACAAA GACTCGCAAG
 3051 CTCGACCTGA CACCCCTCCC AGGAGCGCGT CCTCTGGGGC GCTGACCCAG
 3101 GGGCACCTTA GAGTGGCGCC CGGCTCCGAT CGCTGCCCCCT NNCCCTCCG
 3151 CCAGGGCCAC CTGGGAGCCT CGGGGATGCC CCTTGACCG GCAGAGNGCA
 3201 CGGACTAGGT GGAGGGGNCC GGGATTGGGG CGGGGGGCAG NCAGTTGCCC
 3251 TACAAGTTGG ACCGATGGCC TTGACCTGAT GGCTTCTGGG CGGGGGGCGT
 3301 GGGGAGCTGG GGACCCGGAG CGCACTGGGG ACTGGGGAGG GGCCGCAGCT
 3351 TGGGCCGGAG GGAAGAGGGG ACTTGAAGAA GGGGAGCCCC GCGCGCGCGG
 3401 CTGTGGGCTT GGGGACCGGG GACTTCTCGC GCCATCCCCA GGAACGCCAG
 3451 GCAAGGTCTG GGGAACAAA GAGGAAGCTG CCCCAGAGA GCCGAGCTC
 3501 GACTGNACTC CC 3'

Figure 4

5'

1 CTGGGTGCCG CATGCATCGT GGTGCTCATC TTTCTGGCCT TCCAGCAGAG
 51 GGCATATGTG GCCCTGCCA ACCTGCCTGC TCTCCTGCTG TTGCTACTAC
 101 TGTATGGCTG GTCGATCACA CCGCTCATGT ACCCAGCCTC CTTCTTCTTC
 151 TCCGTGCCCA GCACAGCCTA TGTGGTGCTC ACCTGCATAA ACCTCTTTAT
 201 TGGCATCAAT GGAAGCATGG CCACCTTTGT GCTTGAGCTC TTCTCTGATC
 251 AGAAGCTGCA GGAGGTGAGC CGGATCTTGA AACAGGTCTT CCTTATCTTC
 301 CCCACTTCTG CTTGGGCCGG GGGCTTATTG ACATGGTGCG GNAACCAGGC
 351 CATGGCTGAT GCCTTTGANC CCTTGGGAAA AAGGCAGTTC AAGTACCCTG

Figure 4a

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401 NCTTGGAAGG TGGCGGAAGA ACCTTTTGGC ATGGGAACAG GGCCCCCTTT
451 CCTTCTCTTC ACACTANTGT TCAAGCACCG AAGCCAATC NTGCCACAAG
501 CCCAGGTAAG GTCTCTGCCA CTCCTGGAGA GAGACGAGGA TGTAGCCCGT
551 GAACGGGAGC GGGTGGTCCA AGGAGCCACC CAGGGGGATG TGTTGGTGCT
601 GAGGAACTTG ACCAAGGTAT ACCGTGGGCA GAGGATGCCA GCTGTTGACC
651 GCTTGTGCCT GGGGATTCCC CCTGGTGAGT GTTTTGGGCT GCTGGGTGTG
701 AACGGAGCAG GGAAGACGTC CACGTTTCGC ATGGTGACGG GGGACACATT
751 GGCCAGCAGG GGCGAGGCTG TGCTGGCAGG CCACAGCGGG CCCGGGAACC
801 CAGTGTGCGC ACCTCNAGGG CAGGCNCAGC GTGGCCCCGGG AACCCAGTGC
851 TGCGCACCTA AGCATGGGAT ACTGCCCTNA ATCCGATGCC ATCTTTGAGC
901 TGCTGACGGG CCGCGAGCAC CTGGAGCTGC TTGCGCGCCT GCGCGGTGTC
951 CCGGAGGCCC AGGTTGCCCA NACCGNTGGC TCGGGCCTGG CGCGTCTGGG
1001 ACTCTCATGG TACGCAGACC GGCCTGCAGG CACCTACAGG AACCTGCCCC
1051 GGCGGCCGCT CGAGCCCNNTA NNTGAAGTA 3'

Figure 4b

...CTCCTGCCAC AGTTAGTGAG GTCTATGGAG AGGGTGGCAG GGGCCAAGGA
CCTACTTTAA GCCACAGAT ATTCTGTCCC CAGGCCCAGG GTGAGGTCTC...

Figure 5

CDNA-sequences of lipid sensitive Genes:

ABCB9, ABCA6, ABCC4, ABCA1, ABCD2, ABCB1, ABCB4, ABCC2, ABCD1, ABCC1, ABCB6, ABCB11, ABCG2, ABCC5, ABCA5, ABCG1, ABCA3

ABCB9 GENBANK:U66676

GCCAATGNCACGGTTTCATCATGGAAGTCCAGGACGGCTACAGCACAGAGACAGGGGAGA
AGGGCGCCAGCTGTCAGGTGGCCAGAAGCAGCGGGTGGCCATGGCCGNGGCTCTGGTG
GGAACCCCCCAGTCCTCATCCTGGATGAAGCCACCAGCGCTTTGGATGCCGAGAGCGAGT
ATCTGATCCAGCAGGCCATCCATGGCAACCTGTCAGAAGCACACGGTACTCATCATCGCG
CACCGGCTGAGCACGGTGGAGCACGCGCACCTCATTGTGGTGCTGGACAAGGGCCGCGTA
GTGCAGCAGGGCACCCACCAGCAGCTTGCTTGCCCCAGGGCGGGCTTTTACGGCAAGCTN
GTTGCAGCGGCAGATGTGGGGTTTCAAGGCCGAGACTTCACAGCTGGCCACAACGAGCC
TGTAGCCAAACGGGTCAAGGCCCTGATGGGGGGCCCCCTCCTTCGCCCCGGTGGCAGAGGAC
CCGGTGCCTGCCTGGCAGATGTGCCACGGAGGTTTCCAGCTGCCCTACCGAGCCAGGC
CTGCAGCACTGAAAGACGACCTGCCATGTCCCATGATCACCGCTTNTGCAATCTTGCCCC
TGGTCCCTGCCCCATTCCCAGGGCACTCTTACCCCNNNCTGGGGGATGTCCAAGAGCATA
GTCTCTCTCCCCATACCCCTCCAGAGAAGGGGCTTCCCTGTCCGGAGGGAGACACGGGGAA
CGGGATTTTCCGTCTCTCCCTCTTGCCAGCTCTGTGAGTCTGGCCAGGGCGGGTAGGGAG
CGTGGAGGGCATCTGTCTGCCAATTGCCCGCTGCCAATCTAAGCCAGTCTCACTGTGACC
ACACGAAACCTCAACTGGGGGAGTGAGGAGCTGGCCAGGTCTGGAGGGGCTCAGGTGCC
CCCAGCCCCGGCACCCAGCTTTTCGCCCCCTCGTCAATCAACCCCTGGCTGGCAGCCGCCCTC
CCCACACCCGCCCTGTGCTCTGTCTGTCTGGAGGCCACGTGGACCTTCATGAGATGCATT
CTCTTCTGTCTTTGGTGGANGGGATGGTGCAAAGCCCAGGATCTGGCTTTGCCAGAGGTT
GCAACATGTTGAGAGAACCCGGTCAATAAAGTGTACTACCTCTTACCCCT

ABCA6 GENBANK:U66680

TCTTAGATGAGAAACCTGTTATAATTGCCAGCTGTCTACACAAAGAATATGCAGGCCAGA
AGAAAAGTTGCTTTTCAAAGAGGAAGAAGAAAATAGCAGCAAGAAATATCTCTTTCTGTG
TTCAAGAAGGTGAAATTTTGGGATTGCTAGGACCCAATGGTGCTGGAAAAAGTTCACTA
TTAGAATGATATCTGGGATCACAAAGCCAACCTGCTGGAGAGGTGGAAGTGAAGGCTGCA
GTTCAAGTTTTGGGCCACCTGGGGTACTGCCCTCAAGAGAACGTGCTGTGGCCCATGCTGA
CGTTGAGGGAACACCTGGAGGTGTATGCTGCCGTCAAGGGGCTCAGGAAAGCGGACGCGA
GGCTCGCCATCGCAAGATTAGTGAGTGCTTTCAAAGTGCATGAGCAGCTGAATGTTCTCTG
TGCAGAAATTAACAGCAGGAATCACGAGAAAGTTGTGTTTTGTGCTGAGCCTCCTGGGAA
ACTCACCTGTCTTGCTCCTGGATGAACCATCTACGGGCATAACCCACAGGGCAGCAGCA
AATGTTGGCAGGCAATCCAGGCAGTCGTTAAAAACACAGAGAGAGGTGTCTCTCTGACCA
CCCATAACCTGGCTGAGGCGGAAGCCTTGTGTGACCGTGTGGCCATCATGGTGTCTGGAA
GGCTTAGATGCATTGGCTCCATCCAACACCTGAAAAACAACTTGGAAGGATTACATTC
TAGAGCTAAAAGTGAAGGAAACGTCTCAAGTGACTTTGGTCCCACTGAGATTCTGAAGC

Figure 5a

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TTTTCCACAGGCTGCAGGGCAGGAAAGGTATTCCTCTTTGTAACTATAAGCTGCCCC
GTGGCAGACGTTTACCCTCTATCACAGACCTTTCACAAATTAGAAGCAGTGAAAGCATAA
CTTTAACCTGGAAGAATACAGCCTTCTCCAGTGACACTGGANAAGGTNTCCTTANAAC
CTTCCTAAANAACAGGAAGTTAGGAAATTTTGAATGAAAANNNACNCCCCCCTCATT
AGGTGGAACCTTAAACCTCAAACCTAGTAATTTTTTGTGATCTCCTATAAACTTATG
TTTTATGTAATAATTAATAGTATGTTTAAATTTTAAAGATCATTTAAAATTAACATCAGGT
ATATTTTGTAAATTTAGTTAACAAATACATAAATTTTAAATTTATTCTTCCTCTCAAACA
TAGGGGTGATAGCAAACCTGTGATAAAGGCAATACAAATATTAGTAAAGTCACCCAAAG
AGTCAGGCACTGGGTATTGTGGAATAAACTATATAAACTTAA

ABCC4 GENBANK:U66682

ATGGATAAGTTTATACTAGTGTGGCACATGGCGGCATGTATAGATATACTAGGAGGACC
TAGTTGTATTCTTGTATGAAAAGCGTCCCTGCTACTACAATAAGTCTTTCGTGAAAGG
AGTGTAATCCTAACAACTCAGGAAAGTATTTTGAAAAGAATACTGGATAAGGAAAAA
CCTGCAGCTACTCCTGCTATTTCAAGACATTGCTTACAAGTGGTGGTGTGGTCTCTGTG
GCTGTGGCCGTGATTCTTGGATCGCAATACCCTTGGTTCCCCCTTGAATCATTTTCATT
TTTCTTCGGCGATATTTTTTGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAAGT
GAGTATGGAACTCGGGTTGGTATAGACATGCTAGCTAGTTTCCATTTATGCCATAAATT
ACAGAGACCCCTGAAATTCGGCAGACTCTGTCTCCAGAATTTCTCTAACATTAGGTAA
TTGAACGTATTGGCCATTATGAATCATTGTGTCCCTTAGAGCATGTGGAATTGATAGCCT
GCAACGTGTAACCTTTCATTGGAATAAGGAAGGAGTGAAGGCCATATGGGGAGTAATAT
TCTACAGGAATGTCAGCACTGTGAAGACAGGGACTC

ABCA1 Acc.Nr.: AJ012376 GENBANK:HSA012376

CAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATC
TCTGTTCCGGCTGAGCTACCCACCCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC
ATGCCCTCTGCAGGAACACTTCCTTGGGTTGAGGGGATTATCTGTAATGCCAACACCCC
TGTTTCCGTTACCCGACTCCTGGGGAGGCTCCCGGAGTTGTTGGAACTTTAACAAATCC
ATTGTGGCTCGCCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAAAGACACC
AGCATGAAGGACATGCGCAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA
AACTTGAAGCTTCAAGATTTCTGGTGGACAATGAAACCTTCTCTGGGTTCTGTATCAC
AACCTCTCTCTCCCAAAGTCTACTGTGGACAAGATGCTGAGGGCTGATGTCATTCTCCAC
AAGGTATTTTGAAGGCTACCAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA
GAAGAGATGATTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCCTACCAAGGGAG
AACTGGCTGCAGCAGAGCGAGTACTTGGTTCCAACATGGACATCCTGAAGCCAATCCTG
AGAACAATAAATCTACATCTCCCTTCCCGAGCAAGGAGCTGGCCGAAGCCACAAAAACA
TTGCTGCATAGTCTTGGGACTCTGGCCAGGAGCTGTTAGCATGAGAAGCTGGAGTGAC
ATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC
TACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGGGGCTGAAGATCAAG
TCTCTCAACTGGTATGAGGACAACAATAAAGCCCTCTTTGGAGGCAATGGCACTGAG

Figure 5b

- 12/42 -

GAAGATGCTGAAACCTTCTATGACAACTCTACAACTCCTTACTGCAATGATTTGATGAAG
AATTTGGAGTCTAGTCCTCTTTCCCGCATTATCTGGAAAGCTCTGAAGCCGCTGCTCGTT
GGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCAATGGCTGAGGTGAAC
AAGACCTTCCAGGAACTGGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAACTCAGC
CCCAAGATCTGGACCTTTCATGGAGAACAGCCAAGAAATGGACCTTGTCCGGATGCTGTTG
GACAGCAGGGACAATGACCACTTTTGGGAACAGCAGTTGGATGGCTTAGATTGGACAGCC
CAAGACATCGTGGCGTTTTTGGCCAAGCACCCAGAGGATGTCCAGTCCAGTAATGGTTCT
GTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCAGGCAATCCGGACCATATCTCGC
TTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCCATAGCAACAGAAGTCTGGCTCATC
AACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTGTTCACTGGA
ATTACTCCAGGCAGCATTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATT
GACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACCCTGGTCTCGAGCT
GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG
GAGCAGGCAATCATCAGGGTGTGACGGGCACCGAGAAGAAAATGGTGTCTATATGCAA
CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGAGCCGGTCAATG
CCCCTCTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG
TATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGCATC
CTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCTCTTCTTGTGAGCGCTGGCCTGCTA
GTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTGTC
TTCCTGTCCGTGTTTGTGTGGTGACAATCCTGCAGTGCTTCTGATTAGCACACTCTTC
TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC
TACGTCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC
CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGAGCAG
GGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCTGTGGAGGAAGATGGCTTCAAT
CTCACCCTTCGGTCTCCATGATGCTGTTTGACACCTTCTCTATGGGGTGATGACCTGG
TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATTTCCAGGCCCTGGTATTTTCTTGC
ACCAAGTCTCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACCCTGGTTCCAACCAG
AAGAGAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC
ATTGAGAACCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCTGTGATGGCCTGGCA
CTGAATTTTATGAGGGCCAGATCACCTCCTTCTGGGCCACAATGGAGCGGGGAAGACG
ACCACCATGTCAATCCTGACCGGGTTGTTCCCCCGACCTCGGGCACCGCCTACATCCTG
GGAAAAGACATTGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCCAG
CATAACGTGCTGTTTGACATGCTGACTGTGGAAGAACACATCTGGTTCTATGCCCGCTTG
AAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT
TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTGAGGTGGAATGCAGAGAAAG
CTATCTGTGGCCTTGGCCTTTGTGCGGGGATCTAAGGTTGTCAATCTGGATGAACCCACA
GCTGGTGTGGACCCCTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA
GGCCGCACCATATTCTCTCTACACACCACATGGATGAAGCGGACGTCTGGGGGACAGG
ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC

CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT
TCCTGCAGAAACAGTAGTAGCACTGTGTCTACCTGAAAAAGGAGGACAGTGTCTCTCAG
AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC
TCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCCGGCTGGTGGAAAGACATA
GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTTGTGGAA
CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA
GAGACGACCTTGAAGAAATATTCTCAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG
ACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCGGGGACAAGCAGAGC
TGTCTTCGCCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATTCTGACATAGACCCA
GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGTCTACCAGGTGAAA
GGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTGTGGAAAGAGACTGCTAATTGCC
AGACGGAGTCGGAAAGGATTTTTTGTCTCAGATTGTCTTGCCAGCTGTGTTTGTCTGCATT
GCCCTTGTGTTTCAAGCTGATCGTGCCACCTTTGGCAAAGTACCCAGCCTGGAACCTCAG
CCCTGGATGTACAACGAACAGTACACATTTGTGTCAGCAATGATGCTCCTGAGGACACGGGA
ACCTTGGAACCTCTTAAACGCCCTCACCAAAGACCTGGCTTCGGGACCCGCTGTATGGAA
GGAAACCCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCA
GTTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACTGGACAATGCAGAACCTTCA
CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCAGGG
GCAGGGGGGCTGCCTCCTCCACAAAGAAAACAAACACTGCAGATATCCTTCAGGACCTG
ACAGGAAGAAACATTTCCGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC
TTAAAGAACAAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGT
AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAA
CACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT
ATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCAT
GCAATCAGCTCTTTCTGAATGTCAACAATGCCATTCTCCGGGCCAACCTGCAAAAG
GGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAG
CAGCAGCTCTCAGAGGTGGCTCCGATGACCACATCAGTGGATGTCCTTGTGTCCATCTGT
GTCATCTTTGCAATGTCCTTCGTCCCAGCCAGCTTTGTGCTATTCTGATCCAGGAGCGG
GTCAGCAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCTACTGCTC
TCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACTGGTCAATTATCATC
TTCATCTGCTTCCAGCAGAAGTCCTATGTGTCTCCACCAATCTGCCTGTGCTAGCCCTT
CTACTTTTGTCTGATGGGTGGTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTT
AAGATCCCCAGCACAGCCTATGTGGTGGCTCACCAGCGTGAACCTCTTCATTGGCATTAAAT
GGCAGCGTGGCCACCTTTGTGCTGGAGCTGTTACCGACAATAAGCTGAATAATATCAAT
GATATCCTGAAGTCCGTGTTCTTGATCTTCCACATTTTTGCCTGGGACGAGGGCTCATC
GACATGGTGA AAAACAGGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTT
GTGTCACCAATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGG
GTGGTGTCTTCTCATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCAGACCT
GTAAATGCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGGCGGGAAAGACAG

AGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATA
TATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCATTCTCTCTGGTGAG
TGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAAAATCATCAACTTTCAAGATGTTAACA
GGAGATACCACTGTTACCAGAGGAGATGCTTTCTTAACAGAAATAGTATCTTATCAAAC
ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTG
TTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAA
GTTGGCAAGGTTGGTGAGTGGGCGATTGCGAACTGGGCCTCGTGAAGTATGGAGAAAAA
TATGCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC
GGCGGGCCTCCTGTGGTGTTTCTGGATGAACCCACCACAGGCATGGATCCCCAAAGCCCCGG
CGGTTCTGTGGAATTGTGCCCTAAGTGTGTCAAGGAGGGGAGATCAGTAGTGCTTACA
TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA
AGGTTCAAGGTGCCTTGGCAGTGTCAGCATCTAAAAATAGGTTTGGAGATGGTTATACA
ATAGTTGTACGAATAGCAGGGTCCAACCCGGACCTGAAGCCTGTCCAGGATTTCTTTGGA
CTTGCAATTTCTGGAAGTGTTCAAAAGAGAAACACCGGAACATGCTACAATACCAGCTT
CCATCTTCATTATCTTCTCTGGCCAGGATATTGAGCATCCTCTCCCAGAGCAAAAAGCGA
CTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACCTT
GCCAAGGACCAAAGTGATGATGACCACTTAAAAGACCTCTCATTACAAAAACCAGACA
GTAGTGGACGTTGCAGTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAAGAAAGCTAT
GTATGAAGAATCCTGTTTCATACGGGGTGGCTGAAAGTAAAGAGGGACTAGACTTTCTTT
GCACCATGTGAAGTGTGTGGAGAAAAGAGCCAGAAGTTGATGTGGGAAGAAGTAAACTG
GATACTGTACTGATACTATTCAATGCAATGCAATTCAATG
ABCD2 Acc.Nr.: AJ000327 GENBANK:HSALDR
AAAACACAACAGTGGAAGAGAAACGCTGCATACTATGGGACGCTGTAGGACTTTCTAAAA
CATTTGCTGGGGATTTCTGTGAAGCATGATCTTTTAAACGAATTCTTTTGGAAAGCCGGTT
TGGGTAACTGGGAAAATGACACATATGCTAAATGCAGCAGCTGATCGAGTGAAATGGACC
AGATCGAGTGCTGCTAAGAGGGCTGCCTGCCTGGTGGCTGCGGCATATGCTCTGAAAACC
CTCTATCCCATCATTGGCAAGCGTTTAAAGCAATCTGGCCACGGGAAGAAAAAAGCAGCA
GCTTACCCTGCTGCAGAGAACACAGAAATACTGCATTGCACCGAGACCATTTGTGAAAAA
CCTTCGCCTGGAGTGAATGCAGATTTCTTCAAACAGCTACTAGAACTTCGGAAAAATTTG
TTTCCAAAACCTTGTGACCACTGAAACAGGGTGGCTCTGCCTGCACTCAGTGGCTCTAATC
TCAAGAACCTTTCTTTCTATCTATGTGGCTGGTCTGGATGGAAAAATCGTGAAAAGCATT
GTGGAAAAGAAGCCTCGGACTTTTCATCATCAAATTAATCAAGTGGCTTATGATTGCCATC
CCTGCTACCTTCGTCAACAGTGCAATAAGGTACCTGGAATGCAAATTGGCTTTGGCCTTC
AGAAGTGCCTAGTAGACCACGCCTATGAAACCTATTTTACAAATCAGACTTATTATAAA
GTGATCAATATGGATGGGAGGCTGGCAAACCTGACCAATCTCTTACGGAGGATATTATG
ATGTTCTCCCAATCTGTGGCTCACTTGTATTCCAATCTGACCAAACCTATTTTAGATGTA
ATGCTGACCTCCTATACACTCATTCAAACCTGCTACATCCAGAGGAGCAAGCCCAATTGGG
CCCACCTACTAGCAGGACTTGTGGTGATGCCACTGCTAAAGTGTTAAAGCCTGTTCT
CCCAAATTTGGCAAACCTGGTGGCAGAGGAAGCACATAGAAAAGGCTATTTGCGGTATGTG

CACTCGAGAATTATAGCCAATGTAGAAGAAATTGCCTTTTACAGAGGACATAAGGTAGAA
ATGAAACAACTTCAGAAAAGTTACAAAGCTTTAGCAGATCAGATGAACCTCATTTTATCC
AAACGTTTGTGGTACATCATGATAGAACAGTTCCTGATGAAGTATGTTTGGAGCAGCAGT
GGACTAATTATGGTGGCTATACCTATTATCACTGCAACTGGCTTTGCAGATGGTGAGGAT
GGCCAAAAGCAAGTTATGGTTAGTGAACGGACAGAAGCCTTTACCACTGCTCGAAATTTA
CTGGCCTCTGGAGCTGATGCTATTGAAAGGATTATGTCTTCATACAAAGAGGTCAGTAA
TTAGCAGGCTACACTGCTCGAGTGTACAATATGTTTTGGGTCTTTGATGAAGTAAAAAGA
GGCATTATATAAGAGAACTGCTGTCAATCAAGAATCTGAAAGCCATAGCAAGAAATGGAGCT
AAGGTAGAATTACCTCTCAGTGACACATTGGCAATTAAAGGAAAAGTTATTGATGTGGAT
CACGGAATTATTTGTGAAAATGTTCCCATAAATTACACCAGCAGGAGAAGTGGTGGCTTCC
AGGCTAAACTTCAAAGTAGAAGAAGGAATGCATCTTTTGATAACTGGTCCCAATGGTTGT
GGGAAAAGTTCTCTCTTCAGAAATCTAAGTGGGCTCTGGCCTGTGTATGAAGGAGTCCTC
TATAAACCACTCTCAACATATGTTTTATATTCCACAAAGGCCATATATGTCTCTTGGA
AGTCTTCGGGATCAAGTCATTTACCCTGATTCACTGGATGATATGCATGATAAAGGTTAT
ACAGACCAAGATCTGGAACGTATCCTACACAATGTCCATCTCTATCAGATAGTTCAAAGA
GAAGGAGGATGGGATGCTGTTATGGACTGGAAAGATGTCCTGTCAGGAGGGGAAAAGCAA
AGAATGGGCATGGCTCGTATGTTTTATCATAAACCAAAATATGCCTTGCTGGATGAATGT
ACCACTGCTGTCAGCATTGATGTGGAAGGAAAGATATTTCAAGGCTGCAAAAGGGGCTGGA
ATTTCTTACTGTCTATAACACACAGACCTCTCTTTGGAAATACCACACACATTTATTA
CAGTTTGATGGTGAAGGAGGTTGGCGCTTTGAACAATTGGATACTGCTATCCGTTTGACA
TTGAGTGAAGAAAAACAAAAGCTAGAATCTCAGCTAGCTGGAATTCCTCAAAATGCAGCAG
AGACTCAATGAAGTATGTAAATTTTGGGAGAAGACTCAGTGTGAAAACAATTAAAAAT
GAAGATGAGACATCTTAATTTGTTTTGACATATTTTAAAAAGTTAATTATTAGATAAAGG
CTCAAAGACATTCTGTTATACTGCATGAAGTATGTTAAGCTAAGCACAGAGAAAAAAGG
CAGCAAGACATGTTTTATAAGATTTTAGCATTAAGGAAGTATATGATCTGACTTTTCAGA
AGAAAATAACAAATGCATTATGTAAGGTCAGTCATTATGACTTATACTAATTCCTAGTG
AAGGCCTAATGCACTTGTAACACAGGATTTTCTAGGTGAATTCCTGATGAATACCAGATT
TACTATGTATATGTGGTGTGTCTGAAGTCTTAACAAACATGGGCAATATTCTGGAAATG
AAACAAGTTATACTGAGCACCATTGTTGGGTTGATACCAAGTGCAATAGATTCAAACCTTG
AGTGACATTTAGTCCATTTATGGTTGATATTAGGTTTAAATACCTAGAATTCAAATTGATT
ATTGCTAGTGGCCAACTAAACCTGTACAAAATAGCTGACAGTTTTATACTAATTTCAAT
ATAAAAAATTGTTTTAATGGCATTGTTGAAAGAAAAAGCATGGCTAAAATGTATCAAT
GCCNTATTTTTAAATTTTGGACTTTAAGCATCTTAATGAGGGCATATAACAAATTAATTT
TAGTACAATCTTAAATATTTTAAATAAATCCTTTTCAATTTTAAAAAGAGAATTGCCAATAC
AGAAAAGGAGTATCCAAACATGTCTCAACCTGATAATTCCTTAGCAGAATTACCTATT
GCACTTCTGTTTCAGAAATACACAGCTTGTTTTTTTGGCCAAAGGATGAGTCTACATTTTA
AGAAGTGCATGGTATAAAGGAACCTTAAGGATTCTGAGAATCATAGTAATAACATACATT
GGAATAGTACTTTATAATTTACAATCCCCATTTACATCATTTACCTTAATGTTGAGGAC
AATGTTTTGAAACAAATACTATTTTTCTACTTTTGCTTTTGAGAAAATTGACACTCAGAC

TTGCCCTAATCATGCACTTTACTTAAGGAAAGATCGAGAAATCAAATGAAGTTCTCCTGA
CTCTCTGGTTTAGTGCTCTTTTGTATTATCCTTTAAATCAAACGGGCTATAATAGCAA
TAAAAGTTAGACGAAGGTGTAGAAAATAAAATAAATTTTCATAATGTTAAAAA
AAAAAA

ABCB1 Acc.Nr. M14758 GENBANK:HUMMDR1

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Figure 5g

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ABCB4 Acc. Nr.: M23234 GENBANK:HUMMDR3

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ABCC2 Acc.Nr.: U49248 GENBANK:HSU49248

AGGATAATTCCTGTTCCACTTTCTTTGATGAAACAAGTAAAGAAGAAACAACACAATCAT
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Figure 5j

- 20/42 -

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ABCD1 Acc.Nr.: Z21876 GENBANK:HSXLALDA
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CACCCCGCCCTGCATGCCTGGCCCCCTCCTCCTAGAAAACCCCTTCCCGCC
ABCC1 Acc.Nr.: L05628 GENBANK:HUMMRPX
CCAGGCGGCGTTGCGGCCCCGGCCCCGGCTCCCTGCGCCGCCGCCGCCGCCGCCGCC
GCCGCCGCCGCCGCCGCCAGCGCTAGCGCCAGCAGCCGGGGCCCGATCACCCGCCGCCCGG
TGCCCCGCCGCCGCCGCCAGCAACCGGGCCCGATCACCCGCCGCCCGGTGCCCGCCGC
CGCCCCGCCGCCACCGGCATGGCGCTCCGGGGCTTCTGCAGCGCCGATGGCTCCGACCCGCT
CTGGGACTGGAATGTCACGTGGAATACCAGCAACCCGACTTCACCAAGTGCTTTTCAGAA
CACGGTCTCTGCTGTGGGTGCCTTGTTTTTACCTCTGGGCCTGTTTCCCCTTCTACTTCCT
CTATCTCTCCCGACATGACCGAGGCTACATTGAGATGACACCTCTCAACAAAACCAAAAC
TGCTTGGGATTTTTGCTGTGGATCGTCTGCTGGGCAGACCTCTTCTACTCTTTCTGGGA
AAGAAGTCGGGGCATATTCTGGCCCCAGTGTTTTCTGGTCAGCCCAACTCTCTTGGGCAT
CACCACGCTGCTTGCTACCTTTTTAATTGAGCTGGAGAGGAGGAAGGGAGTTCAGTCTTC
AGGGATCATGCTCACTTTCTGGCTGGTAGCCCTAGTGTGTGCCCTAGCCATCCTGAGATC
CAAAATTATGACAGCCTTAAAGAGGATGCCAGGTGGACCTGTTTCGTGACATCACTTT
CTACGTCTACTTTTCCCTCTTACTCATTGAGCTCGTCTTGTCTGTTTCTCAGATCGCTC
ACCCCTGTTCTCGGAAACCATCCACGACCCTAATCCCTGCCAGAGTCCAGCGCTTCCTT
CCTGTGAGGATCACCTTCTGGTGGATCACAGGGTTGATTGTCCGGGGCTACCGCCAGCC
CCTGGAGGGCAGTGACCTCTGGTCCTTAAACAAGGAGGACACGTGGAACAAGTCGTGCC
TGTTTTGGTAAAGAACTGGAAGAAGGAATGCGCCAAGACTAGGAAGCAGCCGGTGAAGST
TGTGTACTCCTCCAAGGATCCTGCCAGCCGAAAGAGAGTTCCAAGGTGGATGCGAATGA
GGAGGTGGAGGCTTTGATCGTCAAGTCCCCACAGAAGGAGTGAACCCCTCTCTGTTTAA
GGTGTATACAAGACCTTTGGGGCCCTACTTCTCATGAGCTTCTTCTCAAGGCCATCCA
CGACCTGATGATGTTTTCCGGGGCCGAGATCTTAAAGTTGCTCATCAAGTTCGTGAATGA
CACGAAGGCCCCAGACTGGCAGGGCTACTTCTACACCGTGTCTGCTGTTTGTCACTGCCTG
CCTGCAGACCCCTCGTGTGCACCACTACTTCCACATCTGCTTCGTGAGTGGCATGAGGAT
CAAGACCGCTGTCAATTGGGGCTGTCTATCGGAAGGCCCTGGTGATCACCATTGAGCCAG

Figure 5n

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AAAATCCTCCACGGTCGGGGAGATTGTCAACCTCATGTCTGTGGACGCTCAGAGGTTTCAT
GGACTTGGCCACGTACATTAACATGATCTGGTCAGCCCCCTGCAAGTCATCCTTGCTCT
CTACCTCCTGTGGCTGAATCTGGGCCCTTCCGTCTGGCTGGAGTGGCGGTGATGGTCCT
CATGGTGCCCGTCAATGCTGTGATGGCGATGAAGACCAAGACGTATCAGGTGGCCACAT
GAAGAGCAAAGACAATCGGATCAAGCTGATGAACGAAATTCTCAATGGGATCAAAGTGCT
AAAGCTTTATGCCTGGGAGCTGGCAATCAAGGACAAGGTGCTGGCCATCAGGCAGGAGGA
GCTGAAGGTGCTGAAGAAGTCTGCCTACCTGTGAGCCGTGGGCACCTTCACCTGGGTCTG
CACGCCCTTTCTGGTGGCCTTGTGCACATTTGCCGTCTACGTGACCATTGACGAGAAACAA
CATCCTGGATGCCCAGACAGCCTTCGTGTCTTTGGCCTTGTTCAACATCCTCCGGTTTCC
CCTGAACATTCTCCCCATGGTCATCAGCAGCATCGTGCAGGCGAGTGTCTCCCTCAAACG
CCTGAGGATCTTTCTCTCCCATGAGGAGCTGGAACCTGACAGCATCGAGCGACGGCCTGT
CAAAGACGGCGGGGGCAGAACAGCATCACCGTGAGGAATGCCACATTACCTGGGCCAG
GAGCGACCCTCCCACTGAATGGCATCACCTTCTCCATCCCCGAAGGTGCTTTGGTGGC
CGTGGTGGGCCAGGTGGGCTGCGGAAAGTCGTCCCTGCTCTCAGCCCTCTTGGCTGAGAT
GGACAAAGTGGAGGGGCAGTGGCTATCAAGGGCTCCGTGGCCTATGTGCCACAGCAGGC
CTGGATTCAGAATGATTCTCTCCGAGAAACATCCTTTTTGGATGTGAGCTGGAGGAACC
ATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCAGACCTGGAAATCCTGCCCAG
TGGGGATCGGACAGAGATTGGCGAGAAGGGCGTGAACCTGTCTGGGGGCCAGAAGCAGCG
CGTGAGCCTGGCCCGGGCCGTGTACTCCAACGCTGACATTTACCTCTTCGATGATCCCCT
CTCAGCAGTGGATGCCCATGTGGGAAAAACATCTTTGAAAATGTGATTGGCCCCAAGGG
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AGGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTC
CTTCCTCAGCATCTTCCTTTTCATGTGTAACCATGTGTCCGCGCTGGCTTCCAACATTG
GCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACTCAGGAGCACACGAAAGTCCG
GCTGAGCGTCTATGGAGCCCTGGGCATTTACAAGGGATCGCCGTGTTTGGCTACTCCAT
GGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTCTGCACGTGGACCTGCTGCACAG
CATCCTGCGGTACCCCATGAGCTTCTTTGAGCGGACCCCCAGTGGGAACCTGGTGAACCG
CTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCGGAGGTCAAGATGTTTCAT
GGGCTCCCTGTTCAACGTCAATTGGTGCCTGCATCGTTATCCTGCTGGCCACGCCCATCGC
CGCCATCATCATCCCGCCCCCTTGGCCTCATCTACTTCTTCGTCCAGAGGTTCTACGTGGC
TTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGCTCCCCGGTCTATTCCCATTT
CAACGAGACCTTGCTGGGGGTGACGTCATTCGAGCCTTCGAGGAGCAGGAGCGCTTCAT
CCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCCTATTACCCAGCATCGTGGC

Figure 50

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CAACAGGTGGCTGGCCGTGCGGCTGGAGTGTGTGGGCAACTGCATCGTTCTGTTTGCTGC
CCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGTCTGGCTTGGTGGGCCTCTCAGTGT
TTACTCATTGCAGGTCAACACGTACTTGAAGTGGCTGGTTCGGATGTCACTCTGAAATGGA
AACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTATTCAGAGACTGAGAAGGAGGCGCC
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CCCCCAATCAGTGTATACAATACTGCAGGTGAAAAATGGGACAACTTCCAGGGGAAGATT
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CTCTCAGTGTGATTAGTCCAGGGCAGACACTGGCGTTTGTGGGAGCAGTGGATGTGGC
AAAAGCACTAGCATTGAGCTGTTGGAACGTTTCTATGATCCTGATCAAGGGAAGGTGATG
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GTTGCTCTAGACAAAGCCAGAGAGGGTCGGACCTGCATTGTTCATTGCCCATCGCTTGTCC
ACCATCCAGAACGCGGATATCATTGCTGTTCATGGCACAGGGGGTGGTGATTGAAAAGGGG
ACCCATGAAGAACTGATGGCCCCAAAAGGAGCCTACTACAACTAGTCACCACTGGATCC
CCCATCAGTTGACCCAATGCAAGAATCTCAGACACACATGACGCACCACTTACAGGGGTT
GTTTTTAAAGAAAAACAATCCCAGCACGAGGGATTGCTGGGATTGTTTTTTCTTTAAA
GAAGAAATNNNNNTATTTTACTTTTACNNNCNTTTTCTTACATCGGAATCCAANCTAATTT
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GGTCCATGTGAGGGAAAACCCAATGTCAAGTGGCAGCTCAGCCACCACTCAGTGCTTCTC
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GAGGCGGGTCTGTAACAGGCAATCAACAAACGTTTCTTGAGCTAGACCAAGGTGAGATTT
GAAAAGAACAGAGGACTGAAGACCAGCTGTGTTTCTTAATAAATTTGTCTTCAAGTG
AAACCAGCTTCCTTCATCTCTAAGGCTAAGGATAGGGAAAGGGTGGGATGCTCTCANGCT
GAGGGAGGCANAAAGGGAAAGTATTANCATGAGCTTTCCANTTAGGGCTGTTGATTTATG
CTTTAACTTCANANTGAGTGTAGGGTGGTGANNCTA

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GTGGCAGACTCCAAGGTTGGAACTCAGTTTATCCGTGGTGTGTCTGGAGGAGAAAGAAAA
AGGACTAGTATAGGAATGGAGCTTATCACTGATCCTTCCATCTTGTCTTGGATGAGCCT
ACAACTGGCTTAGACTCAAGCACAGCAAATGCTGTCTTTTGCTCCTGAAAAGGATGTCT
AAGCAGGGACGAACAATCATCTTCTCCATTTCATCAGCCTCGATATTCCATCTTCAAGTTG
TTTGATAGCCTCACCTTATTGGCCTCAGGAAGACTTATGTTCCACGGGCCTGCTCAGGAG
GCCTTGGGATACTTTGAATCAGCTGGTTATCACTGTGAGGCCTATAATAACCCTGCAGAC
TTCTTCTTGGACATCATTAAATGGAGATTCCACTGCTGTGGCATTAAACAGAGAAAGAAGAC
TTTAAAGCCACAGAGATCATAGAGCCTTCCAAGCAGGATAAGCCACTCATAGAAAAATTA
GCGGAGATTTATGTCAACTCCTCCTTCTACAAAGAGACAAAAGCTGAATTACATCAACTT

Figure 5s

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TCCGGGGGTGAGAAGAAGAAGATCACAGTCTTCAAGGAGATCAGCTACACCACCTCC
TTCTGTCATCAACTCAGATGGGTTTCCAAGCGTTTCATTCAAAAACCTTGCTGGGTAATCCC
CAGGCCTCTATAGCTCAGATCATTGTACAGTCTGACTGGGACTGGTTATAGGTGCCATT
TACTTTGGGCTAAAAATGATTCTACTGGAATCCAGAACAGAGCTGGGGTTCTCTTCTTC
CTGACGACCAACCAGTGTTCAGCAGTGTTCAGCCGTGGAACCTTTGTGGTAGAGAAG
AAGCTCTTCATACATGAATACATCAGCGGATACTACAGAGTGTCTATTTCCTTGGGA
AAACTGTTATCTGATTTATTACCCATGAGGATGTTACCAAGTATTATATTTACCTGTATA
GTGTACTTCATGTTAGGATTGAAGCCAAAGGCAGATGCCTTCTTCGTTATGATGTTTACC
CTTATGATGGTGGCTTATTCAGCCAGTTCATGGCACTGGCCATAGCAGCAGGTCAGAGT
GTGGTTTCTGTAGCAACACTTCTCATGACCATCTGTTTTGTGTTTATGATGATTTTTTCA
GGTCTGTTGGTCAATCTCACAACCATTGCATCTTGGCTGTCTAGGCTTCAGTACTTCAGC
ATTCCACGATATGGATTTACGGCTTTGCAGCATAATGAATTTTTGGGACAAAACCTTCTGC
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ATTAAAGTTAATAGAACTT

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TCATGGTGAAACACCTCTTGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCT

Figure 5t

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CTTGGGCATTGAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCAT
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Figure 5w

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Figure 5aa

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TGTCAGCTCAACACTGGGCTCGCCCTGCACTGCCAGCAATTCTGGGCCATGTTCTTGAA

Figure 5bb

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GAAGGCCGCATACAGCTGGCGCGAGTGGAAAATGGTGGCGGCACAGGTCCTGGTGCCTCT
GACCTGCGTCACCCCTGGCCCTCCTGGCCATCAACTACTCCTCGGAGCTCTTCGACGACCC
CATGCTGAGGCTGACCTTGGGCGAGTACGGCAGAACCGTCGTGCCCTTCTCAGTTCCCGG
GACCTCCCAGCTGGGTGAGCAGCTGTGAGAGCATCTGAAAGACGCACTGCAGGCTGAGGG
ACAGGAGCCCCGCGAGGTGCTCGGTGACCTGGAGGAGTTCTTGATCTTCAGGGCTTCTGT
GGAGGGGGGGCGGCTTTAATGAGCGGTGCCTTGTGGCAGCGTCCTTCAGAGATGTGGGAGA
GCGCACGGTCGTCAACGCCTTGTTCACAACCAGGCGTACCACTCTCCAGCCACTGCCCT
GGCCGTGCTGGACAACCTTCTGTTCAGCTGCTGTGCGGGCCTCACGCCCTCCATTGTGGT
CTCCAACCTTCCCCCAGCCCCGAGCGCCCTGCAGGCTGCCAAGGACCAGTTTAACGAGGG
CCGGAAGGGATTGACATTGCCCTCAACCTGCTCTTCGCCATGGCATTCTTGGCCAGCAC
GTTCTCCATCCTGGCGGTGAGCGAGAGGGCCGTGCAGGCCAAGCATGTGCAGTTTGTGAG
TGGAGTCCACGTGGCCAGTTTCTGGCTCTCTGCTCTGCTGTGGGACCTCATCTCCTTCT
CATCCCCAGTCTGCTGCTGCTGGTGGTGTAAAGGCCCTTCGACGTGCGTGCCTTCACGCG
GGACGGCCACATGGCTGACACCCTGCTGCTGCTCCTGCTCTACGGCTGGGCCATCATCCC
CCTCATGTACCTGATGAACCTTCTTCTTCTTGGGGGGCGGCCACTGCCTACAGAGGCTGAC
CATCTTCAACATCCTGTGAGGCATCGCCACCTTCTGATGGTCACCATCATGCGCATCCC
AGCTGTAAAACTGGAAGAACTTTCCAAAACCTGGATCACGTGTTCTGGTGCTGCCCAA
CCACTGTCTGGGGATGGCAGTCAGCAGTTTCTACGAGAAGTACGAGACGCGGAGGTACTG
CACCTCCTCCGAGGTGCGCGCCCACTACTGCAAGAAATATAACATCCAGTACCAGGAGAA
CTTCTATGCCTGGAGCGCCCCGGGGGTGCGCCGTTTGTGGCCTCCATGGCCGCCCTCAGG
GTGCGCCTACCTCATCTGCTCTTCTCATCGAGACCAACCTGCTTCAGAGACTCAGGGG
CATCCTCTGCGCCCTCCGGAGGAGGCGGACACTGACAGAATTATACACCCGGATGCCTGT
GCTTCCTGAGGACCAAGATGTAGCGGACGAGAGGACCCGCATCCTGGCCCCCAGCCCGGA
CTCCCTGCTCCACACACCTCTGATTATCAAGGAGCTCTCCAAGGTGTACGAGCAGCGGGT
GCCCCCTCCTGGCCGTGGACAGGCTCTCCCTCGCGGTGCAGAAAGGGGAGTGCTTCGGCCT
GCTGGGCTTCAATGGAGCCGGGAAGACCACGACTTTCAAAATGCTGACCGGGGAGGAGAG
CCTCACTTCTGGGGATGCCTTTGTGCGGGGTACAGAAATCAGCTCTGATGTGCGAAAGGT
GCGGCAGCGGATCGGCTACTGCCCCAGTTTGATGCCTTGCTGGACCACATGACAGGCCG
GGAGATGCTGGTCAATGTACGCTCGGCTCCGGGGCATCCCTGAGCGCCACATCGGGGCCCTG
CGTGGAGAACTCTGCGGGCCTGCTGCTGGAGCCACATGCCAACAAGCTGGTCAGGAC
GTACAGTGGTGGTAACAAGCGGAAGCTGAGCACCGGCATCGCCCTGATCGGAGAGCCTGC
TGTCACTTCTCCTGGACGAGCCGTCCACTGGCATGGACCCCGTGGCCCGGCGCCTGCTTTG
GGACACCGTGGCAGGAGCCCGAGAGTCTGGCAAGGCCATCATCATCACCTCCACAGCAT
GGAGGAGTGTGAGGCCCTGTGCACCCGGCTGGCCATCATGGTGCAGGGGAGTTCAAGTG
CCTGGGCAGCCCCCAGCACTCAAGAGCAAGTTGGCAGCGGCTACTCCCTGCGGGCCAA
GGTGCAGAGTGAAGGGCAACAGGAGGCGCTGGAGGAGTTCAAGGCCTTCGTGGACCTGAC
CTTTCAGGCAGCGTCTGGAAGATGAGCACCAGGCATGGTCCATTACCACCTGCCGGG
CCGTGACCTCAGCTGGGCGAAGGTTTTCGGTATTCTGGAGAAAGCCAAGGAAAAGTACGG
CGTGGACGACTACTCCGTGAGCCAGATCTCGCTGGAACAGGTCTTCTGAGCTTCGCCCCA

CCTGCAGCCGCCACCGCAGAGGAGGGGCGATGAGGGGTGGCGGCTGTCTCGCCATCAGG
CAGGGACAGGACGGGCAAGCAGGGCCCATCTTACATCCTCTCTCTCCAAGTTTATCTCAT
CCTTTATTTTTTAATCACTTTTTTCTATGATGGATATGAAAAATTCAAGGCAGTATGCACA
GAATGGACGAGTGCAGCCAGCCCTCATGCCAGGATCAGCATGCGCATCTCCATGTCTG
CATACTCTGGAGTTCACTTTCCAGAGCTGGGGCAGGCCGGGCAGTCTGCGGGCAAGCTC
CGGGGTCTCTGGGTGGAGAGCTGACCCAGGAAGGGCTGCAGCTGAGCTGGGGGTGAATT
TCTCCAGGCACTCCCTGGAGAGAGGACCCAGTGACTTGTCCAAGTTTACACAGCACTA
ATCTCCCTGGGGAGGAAGCGGGAAGCCAGCCAGGTTGAACTGTAGCGAGGCCCCCAGGC
CGCCAGGAATGGACCATGCAGATCACTGTCACTGGAGGGAAGCTGCTGACTGTGATTAGG
TGCTGGGGTCTTAGCGTCCAGCGCAGCCCGGGGSCATCCTGGAGGCTCTGCTCCCTTAGG
GCATGGTAGTCACCGGAAGCCGGGCACCGTCCACAGCATCTCCTAGAAGCAGCCGGCA
CAGGAGGGAAGGTGGCCAGGCTCGAAGCAGTCTCTGTTTCCAGCACTGCACCCCTCAGGAA
GTGCCCCGCCCCAGGACACGCAGGGACCACCTAAGGGCTGGGTGGCTGTCTCAAGGACA
CATTGAATACGTTGTGACCATCCAGAAAAATAATGCTGAGGGGACACAAAAA
AAAAA

Fragment 640918

1 GAGATCCTGAGGCTTTTCCCCCAGGCTGCTCAGCAGGAAAGGTTCTCCTCCCTGATGGTC
61 TATAAGTTGCCTGTTGAGGATGTGCGACCTTTATCACAGGCTTCTTCAAATTAGAGATA
121 GTTAAACAGAGTTTCGACCTGGAGGAGTACAGCCTCTCACAGTCTACCTGGAGCAGGTT
181 TTCCTGGAGCTCTCCAAGGAGCAGGAGCTGGGTGATCTTGAAGAGGACTTTGATCCCTCG
241 GTGAAGTGGAACTCCTCCTGCAGGAAGAGCCTTAAAGCTCCAAATACCTTATATCTTTC
301 TTTAATCCTGTGACTCTTTTAAAGATAATATTTTATAGCCTTAATATGCCTTATATCAGA
361 GGTGGTACAAAATGCATTTGAACTCATGCAATAATTATC

Fragment 698739

1 GCTCTCCACACAGAGATTTTGAAGCTTTTCCACAGGCTGCTTGGCAGGAAAGATATTCC
61 TCTTTAATGGCGTATAAGTTACCTGTGGAGGATGTCCACCTCTATCTCGGGCCTTTTTC
121 AAGTTAGAGGCGATGAAACAGACCTTCAACCTGGAGGAATACAGCCTCTCTCAGGCTACC
181 TTGGAGCAGGTATTCTTAGAACTCTGTAAAGAGCAGGAGCTGGGAAATGTTGATGATAAA
241 ATTGATACAACAGTTGAATGGAACTTCTCCACAGGAAGACCCTTAAATGAAGAACCT
301 CCTAACATTCAATTTTAGGTCCTACTACATTGTTAGTTTCCATAATTCTACAAGAATGTT
361 TCCTTTTACTTCAGTTAACAAAAGAAAAATTTAATAAACATTCAATAATGATTACAGTT
421 TTCATTTTAAAAATTTAGGATGAAGGAAACAAGGAAATATAGGGAAAAGTAGTAGACA
481 AATTAACAAAATCAGACATGTTATTCAATCCCAACATGGGTCTATTTTGTGCTTAAAAAT
541 AATTTAAAAATCATACAATATTAGGTTGGTTATCG

Fragment 990006

1 GTGGAAGATGTGCAACCTTTAGCCCAAGCTTTCTTCAAATTAGAGAAGGTTAAACAGAGC
61 TTTGACCTAGAGGAGTACAGCCTCTCACAGTCTACCTGGAGCAGGTTTTCTGGAGCTC
121 TCCAAGGAGCAGGAGCTGGGTGATTTTGAGGAGGATTTTGATCCCTCAGTGAAGTGAAG

Figure 5dd

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181 CTCCTCCCCCAGGAAGAGCCTTAAAACCCCAAATTCTGTGTTCCCTGTTTAAACCCGTGGT
241 TTTTTTTTAAATACATTTATTTTTATAGCAGCAATGTTCTATTTTTAGAACTATATTATA

Fragment 1133530

1 TTTTCAGTTG CATGTAATAC CAAGAAATCG AATTGTTTTTC CGGTTCTTAT
51 GGGAAATTGTT AGCAATGCCC TTATTGGAAT TTTTAACTTC ACAGAGCTTA
101 TTCAAATGGA GAGCACCTTA TTTTTCGTG ATGACATAGT GCTGGATCTT
151 GGTTTTATAG ATGGGTCCAT ATTTTGTGTTG TTGATCACAA ACTGCATTTC
201 TCCTTATATT GGCATAAGCA GCATCAGTGA TTATT

Fragment 1125168

CTGGATT

TGCTCTGCGG CAAGACCCGC GCCACCAGCG GCAGTATCCA GTTCGACGGC
CAGGAACTGA CCAAAATGCG CGAATACAAC ATCGTGCGGG CCGGGGTAGG
GCGCAAGTTT CAGAACCCGT CGATCTACGA AAACCTCAGG GTGTTTGAAA
ACCTTGAGAT GTCTTATCCG GCTGGGCGCA AGGTCTGGGG TCGCTGTTT
TTCAAGCGCA ATGCCCAGGT GGTGGCGCGG GTCGAG

Fragment 1203215

1 ATCGCCGATA TCTCCCCTTC GGGCTGCGGC AAGAGCACCT TCCTGAAAGT
51 GCTCGCCGGG TTCTATGCCC TGGACACCGG GCGCTTCAGG ATCAACGGCC
101 AGGCGATGCG GCATTTCTGGT TTGCGCTCGT ACCGCCAGAG CGTGGCCTAT
151 GTCACGGCCC ACGACGAGAT CATCGCCGGG ACGGTGATCG AGAACATCCT
201 GATGGACAGC GACCCGCTGG ACGGCACGGG TTTGCAGAGC TGTGTCGAGC
251 AGGCCGGGTT GCTGGAAAGC ATCCTGAAAC TGAGCAATGG CTTCAATACC
301 TTGCTCGGAC CCATGGGCGT GCAATTGTCC TCGGGCCAGA AGCAACGCCT
351 GTTGATCGCC CGGGGTCGAC GC

Fragment 168043

1 AAAACCAAAG ATTCTCCTGG AGTTTTCTCT AAACCTGGGTG TTCTCCTGAG
51 GAGAGTTGAC AAGAACTTG GTGAGAAATA AGCTGGCAGT GATTACGCGT
101 CTCCTTCAGA ATCTGATCAT GGGTTTGTTC CTCCTTTTCT TCGTTCTGCG
151 GGTCCGAAGC AATGTGCTAA AGGGTGCTAT CCAGGACCGC GTAGGTCTCC
201 TTTACCAGTT TGTGGGCGCC ACCCCGTACA CAGGCATGCT GAACGCTGTG
251 AATCTGTTTC CCGTGCTGCG AGCTGTCAGC A

Huwhite2

1 ATGGCCGTGA CGCTGGAGGA CGGGGCGGAA CCCCCTGTGC TGACCACGCA
51 CCTGAAGAAG GTGGAGAACC ACATCACTGA AGCCAGCGC TTCTCCCACC
101 TGCCCAAGCG CTCAGCCGTG GACATCGAGT TCGTGGAGCT GTCCTATTCC
151 GTGCGGGAGG GGCCCTGCTG GCGCAAAAGG GGTATAAGA CCCTTCTCAA
201 GTGCCTCTCA GGTAAATTCT GCCGCCGGGA GCTGATTGGC ATCATGGGCC
251 CCTCAGGGGC TGGCAAGTCT ACATTCATGA ACATCTTGGC AGGATACAGG
301 GAGTCTGGA TGAAGGGGCA GATCCTGGTT AATGGAAGGC CACGGGAGCT

351 GAGGACCTTC CGCAAGATGT CCTGCTACAT CATGCAAGAT GACATGCTGC
401 TGCCGCACCT CACGGTGTTG GAAGCCATGA TGGTCTCTGC TAACCTGAAT
451 CTTACTGAGA ATCCCGATGT GAAAAACGAT CTCGTGACAG AGATCCTGAC
501 GGCACCTGGGC CTGATGTCGT GCTCCACAC GAGGACAGCC CTGCTCTCTG
551 GCGGGCAGAG GAAGCGTCTG GCCATCGCCC TGGAGCTGGT CAACAACCCG
601 CCTGTCAATG TCTTTGATGA GCCCACCAGT GGTCTGGATA GCGCCTCTTG
651 TTTCCAAGTG GTGTCCCTCA TGAAGTCCCT GGCACAGGGG GGCCGTACCA
701 TCATCTGCAC CATCCACCAG CCCAGTGCCA AGCTCTTTGA GATGTTTGAC
751 AAGCTCTACA TCCTGAGCCA GGGTCAGTGC ATCTTCAAAG GCGTGGTCAC
801 CAACCTGATC CCCTATCTAA AGGGACTCGG CTTGCATTGC CCCACCTACC
851 ACAACCCGGC TGAATTCAGT GAGTGGGGGT CTGTTGCCTC TGGCGAGTAT
901 GGACACCTGA ACCCCATGTT GTTCAGGGCT GTGCAGAATG GGCTGTGCGC
951 TATGGCTGAG AAGAAGAGCA GCCCTGAGAA GAACGAGGTC CCTGCCCCAT
1001 GCCCTCCTTG TCCTCCGGAA GTGGATCCCA TTGAAAGCCA CACCTTTGSC
1051 ACCAGCACCC TCACACAGTT CTGCATCCTC TTCAAGAGGA CCTTCCTGTC
1101 CATCCTCAGG GACACGGTCC TGACCCACCT ACGGTTTCATG TCCCACGTGG
1151 TTATTGGCGT GCTCATCGGC CTCCTCTACC TGCATATTGG CGACGATGCC
1201 AGCAAGGTCT TCAACAACAC CGGCTGCCTC TTCTTCTCCA TGCTGTTCTC
1251 CATGTTGCGC GCCCTCATGC CAACTGTGCT CACCTTCCCC TTAGAGATGG
1301 CGGTCTTCAT GAGGGAGCAC CTCAACTACT GGTACAGCCT CAAAGCGTAT
1351 TACCTGGCCA AGACCATGGC TGACGTGCCC TTTCAGGTGG TGTGTCCGGT
1401 GGTCTACTGC AGCATTGTGT ACTGGATGAA CGGCCAGCCC GCTGAGACCA
1451 GCCGCTTCCT GCTCTTCTCA GCCCTGGCCA CCGCCACCGC CTTGGTGGCC
1501 CAATCTTTGG GGCTGCTGAT CGGAGCTGCT TCCAACCTCC TACAGGTGGC
1551 CACTTTTGTG GGCCAGTTA CCGCCATCCC TGTCTCTTG TTCTCCGGCT
1601 TCTTTGTCAG CTTCAAGACC ATCCCCACTT ACCTGCAATG GAGCTCCTAT
1651 CTCTCCTATG TCAGGTATGG CTTTGAGGGT GTGATCCTGA CGATCTATGG
1701 CATGGAGCGA GGAGACCTGA CATGTTTAGA GGAACGCTGC CCGTTCGGG
1751 AGCCACAGAG CATCCTCCGA GCGCTGGATG TGGAGGATGC CAAGCTCTAC
1801 ATGGACTTCC TGGTCTTGGG CATCTTCTTC CTAGCCCTGC GGCTGCTGGC
1851 CTACCTTGTTG CTGCGTTACC GGGTCAAGTC AGAGAGATAG AGGCTTGCCC
1901 CAGCCTGTAC CCCAGCCCCT GCAGCAGGAA GCCCCAGTC CCAGCCCTTT
1951 GGGACTGTTT TANTCTATA CACTTGGGCA CTGGTTCCTG GCGGGGCTAT
2001 CCTCTCCTCC CTTGGCTCCT CCACAGGCTG GCTGTGCGAC TGGCTCCCA
2051 GCCTGGGCTC TGGGAGTGGG GGCTCCAACC CTCCCCACTA TGCCAGGAG
2101 TCTTCCCAAG TTGATGCGGT TTGTAGCTTC CTCCCTACTC TCTCCAACAC
2151 CTGCATGCAA AGACTACTGG GAGGCTGCTG CCTCCTTCCT GCCCATGGCA
2201 CCCTCCTCTG CTGTCTGCCT GGGAGCCCTA GGCTCTCTAT GGCCCCACTT
2251 ACAACTGA

Figure 5ff

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Fragment 20237

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1  TTTAAGGATT TCAGCCTTTC CATTCCGTCA GGATCTGTCA CGGCACTGGT TGGCCCAAGT
61  GGTTCTGGCA AATCAACAGT GCTTTCACCTC CTGCTGAGGT TGTACGACCC TGCTTCTGGA
121 ACTATTAGTC TTGATGGCCA TGACAATCCG TCAGCTAAAC CCAGTGTGTG GCTGAGATCC
181 AAAATTGGGA CAGTCAGTCA GGAACCCATT TTGTTTTCTT GCTCTATTGC TGAGAACATT
241 GCTTATGGTG CTGATGACCC TTCCTCTGTG ACCGCTGAGG AAATCCAGAG AGTGGCTGAA
301 GTGGCCAATG CAGTGGCTTC TCCGGAATTT CCCCCAAGGT TCAACACTGT GGTGGAGAA
361 AAGGGTGTTC TCCTCTCAGG TGGGCAGAAA CAGCGGATTG CGATTGCCCC TGCTCTGCTA
421 AAGAATCCCA AAATTCTTCT CCTAGATGAA GCAACCAGTG CGCTGGATGC CGAAAATGAG
481 TACCTTGTTT AAGAAGCTCT AGATCGCCTG ATGGATGGAA GAACGGTGTT AGTTATTGCC
541 CATAGCCTGT CCACCATTAA GAATGCTAAT ATGGTTGCTG TTCTTGACCA AGGAAAAATT
601 ACTGAATATG GAAAACATGA AGAGCTGCTT TCAAAACCAA ATGGGATATA CAGAAAATA
661 ATGAACAAAC AAAGTTTTAT TTCAGCATAA GGAAGCAATT ACTGGTAAAC AATATGAGAC
721 TTTAATGCAA AACAGTGTG CGAAAAAAA CTCAGAGACT ATGAAATACA TAAACCATAT
781 ATCAAGTTAT TTGAAAAATA CCTATTTTTT CCAAAGTGTG
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